Classify Sequences with Kraken

Kraken is a taxonomic sequence classifier that assigns taxonomic labels to short DNA reads. It does this by examining the k-mers within a read and querying a database with those.

Parameters in GUI

Parameter	Description	Defaultvalue
Input data	To classify single-end (SE) reads or contigs, received by reads de novo assembly, set this parameter to "SE reads or contigs". To classify paired-end (PE) reads, set the value to "PE reads". One or two slots of the input port are used depending on the value of the parameter. Pass URL(s) to data to these slots. The input files should be in FASTA or FASTQ formats.	SE reads or contigs
Database	A path to the folder with the Kraken database files.	
Quick operation	Stop classification of an input read after the certain number of hits. The value can be specified in the "Minimum number of hits" parameter.	False
Load database into memory	Load the Kraken database into RAM (--preload). This can be useful to improve the speed. The database size should be less than the RAM size. The other option to improve the speed is to store the database on ramdisk. Set this parameter to "False" in this case.	True
Number of threads	Use multiple threads (--threads).	8
Output file	Specify the output file name.	auto

Parameters in Workflow File
Type: kraken-classify

Parameter	Parameter in the GUI	Type
input-data	**Input data**	*string*
database	**Database**	*string*
quick-operation	**Quick operation**	*bool*
preload	**Load database into memory**	*bool*
threads	**Number of threads**	*number*
output-url	**Output file**	*string*

Input/Output Ports

The element has 1 *input port*:

Name in GUI: Input sequences:

URL(s) to FASTQ or FASTA file(s) should be provided. In case of SE reads or contigs use the "Input URL 1" slot only.

In case of PE reads input "left" reads to "Input URL 1", "right" reads to "Input URL 2". See also the "Input data" parameter of the element.

Name in Workflow File: in

Slots:

SlotInGUI	Slot in Workflow File	Type
Input URL	**url**	*string*

The element has 1 *output port*:

Name in GUI: Kraken Classification:

A map of sequence names with the associated taxonomy IDs, classified by Kraken.

Name in Workflow File: out

Slots:

SlotInGUI	Slot in Workflow File	Type
Taxonomy classification data	tax-data	*tax-classification*